SEQUENCE LISTING

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Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu Asn 50 55 60

Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys Asn Tyr Glu His Leu 65 70 75 80

Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln Ser 85 90 95

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Gly Leu Leu Ser Leu Gln Val Leu His Glu Glu Thr Ser Gly Cys Lys
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Glu Glu Val Lys Pro Phe Ser Gly Thr Thr Pro Ser Arg Lys Pro Leu 65 70 75 80

Pro Lys Arg Lys Asn Thr Trp Asn Phe Leu Lys Cys Ala Tyr Met Val 85 90 95

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Ser Leu Gly Gln Gly Ala Gly Glu Val Trp Leu Arg Val Asp Cys Arg
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Asn Thr Asp Gln Thr Tyr Trp Cys Glu Tyr Arg Gly Gln Pro Ser Met 65 70 75 80

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Gln Glu Leu Arg Arg Leu His His Ala Cys Gln Gly Ala Pro Val Leu

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Arg Pro Ser Val Cys Arg Glu Ala Gly Pro Gln Ala His Met Gln Gln
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Val Thr Ser Ser Leu Lys Gly Ser Pro Glu Pro Asn Gln Gln Pro Glu 130 135 140

Ala Gly Thr Pro Ser Leu Ser Pro Lys Ala Thr Val Lys Leu Thr Gly
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Ala Thr Gln Leu Gly Lys Asp Ser Met Glu Glu Leu Gly Lys Ala Lys 165 170 175

Pro Thr Thr Gly Pro Thr Ala Lys Pro Thr Gln Pro Gly Pro Arg Pro 180 185 190

Gly Gly Asn Glu Glu Ala Lys Lys Lys Ala Trp Glu His Cys Trp Lys 195 200 205

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Gln Ala Glu Leu Ser Arg Thr Gly Arg Ser Arg Glu Val Leu Glu Leu 50 55 60

Gly Gln Val Leu Asp Thr Gly Lys Arg Lys Arg His Val Pro Tyr Ser
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Val Ser Glu Thr Arg Leu Glu Glu Ala Leu Glu Asn Leu Cys Glu Arg 85 90 95

Ile Leu Asp Tyr Ser Val His Ala Glu Arg Lys Gly Ser Leu Arg Tyr 100 105 110

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Glu Glu Phe Glu Asp Ile Val Gly Asp Trp Tyr Phe His His Gln Glu 165 170 175

Gln Pro Leu Gln Asn Phe Leu Cys Glu Gly His Val Leu Pro Ala Ala 180 185 190

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Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu His 50 55 60

Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val Pro
65 70 75 80

Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Ile Leu Cys 85 90 95

Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln Gly
100 105 110

Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe Lys 115 120 125

Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Glu Leu Met 130 135 140

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Gln Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Pro Lys Gly Thr
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Ile Thr Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Thr Phe 65 70 75 80

Leu Thr Ser Lys Asp Glu Gly Leu Lys Ala Thr Thr Asp Val Arg
85 90 95

Lys Asn Asp Ser Ile Ile Ser Asn Val Thr Val Thr Ser Val Thr Leu
100 105 110

Pro Asn Ala Val Ser Thr Leu Gln Ser Ser Lys Pro Lys Thr Glu Thr
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Gln Ser Ser Ile Lys Thr Thr Glu Ile Pro Gly Ser Val Leu Gln Pro 130 135 140

Asp Ala Ser Pro Ser Lys Thr Gly Thr Leu Thr Ser Ile Pro Val Thr 145 150 155 160

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Lys Asn Ala Ser Thr Ser Ala Thr Ser Arg Ser Tyr Ser Ser Ile Ile
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Leu Val Gly Leu Tyr Arg Met Cys Trp Lys Ala Asp Pro Gly Thr Pro 210 215 220

Glu Asn Gly Asn Asp Gln Pro Gln Ser Asp Lys Glu Ser Val Lys Leu 225 230 235 240

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Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp Ser 100 105 110

Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys Thr Phe
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Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr 145 150 155 160

Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile
165 170 175

Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His
180 185 190

Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu
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Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly 210 215 220

Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu 225 230 235 240

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Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile Ser Thr 20 25 30

Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile 35 40 45

Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu
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Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn 65 70 75 80

Leu Leu Ala Phe Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro 85 90 95

Asn Pro Lys Ile Leu Arg Lys Ile Ile Ser Ile Cys Gln Leu Phe Pro 100 105 110

Leu His Ala Glu Asn Ser Ala Ala Met Cys Glu Ser Leu Gly Gln Asn 115 120 125

Ser Ser Ile Cys Ser Leu Ser Ala Gln Gly Glu Ala Arg Lys Cys Trp 130 135 140

Pro Pro Ser Ala Ser 145

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Ala Thr Ile Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Val 35 40 45

Phe Leu Glu Gln Arg Leu Pro Glu Ile Asn Leu Asp Gly Met Val Gly

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50 55 60

Val Arg Val Leu Glu Glu Gln Leu Lys Ser Val Arg Glu Lys Trp Ala 65 70 75 80

Gln Glu Pro Leu Gln Pro Leu Ser Leu Arg Val Gly Met Leu Gly
85 90 95

Glu Lys Leu Glu Ala Ala Ile Gln Arg Ser Leu His Tyr Leu Lys Leu 100 105 110

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Ser Gln Thr Ser Ala Gly Ala Ser 130 135

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His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys 35 40 45

Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg 50 55 60

Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
65 70 75 80

Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val

Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr

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Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val Val Thr Leu Thr
50 55 60

Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln His Gly Leu Gly Gly 65 70 75 80

Cys Asp Gln Ser Val Met Asp Leu Ile Lys Arg Asn Ser Gly Trp Val 85 90 95

Phe Glu Asn Pro Ser Ile Gly Val Leu Glu Leu Trp Val Leu Ala Thr 100 105 110

Asn Phe Arg Asp Tyr Ala Ile Ile Phe Thr Gln Leu Glu Phe Gly Asp 115 120 125

Glu Pro Phe Asn Thr Val Glu Leu Tyr Ser Leu Thr Glu Thr Ala Ser 130 135 140

Gln Glu Ala Met Gly Leu Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe 145 150 155 160

Leu Ser Gln

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Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln
20 25 30

Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg
35 40 45

Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile 50 55 60

Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu 65 70 75 80

Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val Phe 85 90 95

Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met



100 105 110

Lys Ser Val Leu Trp Trp Leu Pro Val Glu Lys Ala Phe Trp Arg Gln
115 120 125

Pro Ala Gly Pro Gly Ser Gly Ile Arg Glu Arg Leu Glu His Pro Val 130 135 140

Leu His Val Ser Trp Asn Asp Ala Arg Ala Tyr Cys Ala Trp Arg Gly
145 150 155 160

Lys Arg Leu Pro Thr Glu Glu Glu Trp Glu Phe Ala Ala Arg Gly Gly
165 170 175

Leu Lys Gly Gln Val Tyr Pro Trp Gly Asn Trp Phe Gln Pro Asn Arg 180 185 190

Thr Asn Leu Trp Gln Gly Lys Phe Pro Lys Gly Asp Lys Ala Glu Asp 195 200 205

Gly Phe His Gly Val Ser Pro Val Asn Ala Phe Pro Ala Gln Asn Asn 210 215 220

Tyr Gly Leu Tyr Asp Leu Leu Gly Asn Val Trp Glu Trp Thr Ala Ser 225 230 235 240

Pro Tyr Gln Ala Ala Glu Gln Asp Met Arg Val Leu Arg Gly Ala Ser 245 250 255

Trp Ile Asp Thr Ala Asp Gly Ser Ala Asn His Arg Ala Arg Val Thr
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Tyr Met Met Asn Arg

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Ser Ala Leu Ser Cys Ala Arg Thr Gly Ala Pro Ser Cys Pro Arg Arg 50 55 60

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Lys Gly Lys Arg Pro Asn Leu Lys Val His Ile Asn Thr Thr Ser Asp 35 40 45

Ser Ile Leu Leu Lys Phe Leu Arg Pro Ser Pro Asn Val Lys Leu Glu 50 60

Gly Leu Leu Gly Tyr Gly Ser Asn Val Ser Pro Asn Gln Tyr Phe
65 70 75 80

Pro Leu Pro Ala Glu Gly Lys Phe Thr Glu Ala Ile Val Asp Ala Glu 85 90 95

Pro Lys Tyr Leu Ile Val Val Arg Pro Ala Pro Pro Pro Ser Gln Lys
100 105 110

Lys Ser Cys Ser Gly Lys Thr Arg Ser Arg Lys Pro Leu Gln Leu Val 115 120 125

Val Gly Thr Leu Thr Pro Ser Ser Val Phe Leu Ser Trp Gly Phe Leu

130 140

Ile Asn Pro His His Asp Trp Thr Leu Pro Ser His Cys Pro Asn Asp 145 150 Arg Phe Tyr Thr Ile Arg Tyr Arg Glu Lys Asp Lys Glu Lys Lys Trp Ile Phe Gln Ile Cys Pro Ala Thr Glu Thr Ile Val Glu Asn Leu Lys 185 Pro Asn Thr Ser Leu 195 <210> 16 <211> 378 <212> DNA <213> Homo sapiens <400> 16 atggccaagt acctggccca gatcattgtg atgggcgtgc aggtggtggg cagggccttt 60 gcacgggcct tgcggcagga gtttgcagcc agccgggccg cagctgatgc ccgaggacgc 120 gctggacacc ggtctgcagc cgcttccaac ctctccggcc tcagcctcca ggaggcacag 180 cagattetea aegtgteeaa getgageeet gaggaggtee agaagaacta tgaacaetta 240 tttaaggtga atgataaatc cgtgggtggc tccttctacc tgcagtcaaa ggtggtccgc 300 gcaaaggagc gcctggatga ggaactcaaa atccaggccc aggaggacag agaaaaaggg 360 cagatgcccc atacgtga 378 <210> 17 <211> 366 <212> DNA <213> Homo sapiens <400> 17 atgeacagat cagagecatt tetgaaaatg tegetgetga ttetgetttt cetgggattg 60 gcagaagcct gtactcctcg tgaagtcaac ttgctgaaag ggatcatagg tctcatgagc 120 agactgtcac cggatgagat cctaggcttg ctgagcctcc aagtactgca tgaagaaaca 180 agtggctgca aggaggaagt taaaccette teaggeacea ceceateeag gaaaceacte 240 cccaagagga agaacacgtg gaacttcctg aaatgcgcct acatggtgat gacctacctc 300 ttcgtateet acaacaaagg ggactggtte acttttteet eecaagtgtt actgeeacta 360 ctgtaa 366 <210> 18 <211> 672 <212> DNA <213> Homo sapiens <400> 18 atgaagtteg teecetgeet cetgetggtg acettgteet geetggggae tttgggteag 60 gccccgaggc aaaagcaagg aagcactggg gaggaattcc atttccagac tggagggaga 120 gattcctgca ctatgcgtcc cagcagcttg gggcaaggtg ctggagaagt ctggcttcgc 180 gtcgactgcc gcaacacaga ccagacctac tggtgtgagt acagggggca gcccagcatg 240 tgccaggctt tcgctgctga ccccaaatct tactggaatc aagccctgca ggagctgagg 300

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aaaccaagag atgggaatga agaggaatgt gctgtaaaga agagttgtca attgtgcaca 180
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acatcagceg cegegtggce geetteeget ttgagetgeg egaggaeggg egeeeegage 180
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gtccacatca ataccacaag tgactccatc ctcttgaagt tcttgcgtcc aagtccaaat 180
gtaaagcttg aaggtcttct cctgggatat ggcagcaatg tatcaccaaa ccagtacttc 240
cctcttcccg ctgaagggaa attcacagaa gctatagttg atgcagagcc gaaatatctg 300
atagttgtgc gacctgctcc acctccaagt caaaagaagt catgttcagg taaaactcgt 360
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agattttata caattcgcta tcgagaaaag gataaagaaa agaagtggat ttttcaaatc 540
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atgaagttcg tcccctgcct cctgc
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value descripcion of intelligial dequence. Illimer	
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tcaaagatct tctcggtcaa gtttg	25
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27.0		
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<223> Description of Artificial Sequence: Synthetic FLAG
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<400> 71
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